evolutionary relationships between the plant host, seed-borne pathogens and seed-associated microbiota have been overlooked so far. Here, we analyzed for the first time the microbial turnover in seeds of a forest tree species (*Quercus petraea*), using a hierarchical sampling design including three spatial scales (seed micro-environment, mother tree and forest site). A total of 125 acorns, collected either in the canopy or on the ground, were analyzed. The microbiota in the microenvironment of each seed (formed by twigs and leaves, or litter and soil, respectively) was also characterized. We focused on the fungal component of the microbial community as *Q. petraea* often hosts seed-borne fungal pathogens (*Ciboria* sp.). We combined a metabarcoding approach with quantitative PCR to characterize the richness, composition and abundance of the fungal community. Our results revealed significant effects of the mother tree and forest site on the fungal community of the acorns that are in the canopy. Interestingly, the maternal effects disappear when acorns fall on the ground as seed-borne fungal taxa are largely replaced by soil-borne taxa. Future analyses using Hierarchical Modelling of Species Communities (HMSC) will enable us to highlight the associations between seed-borne pathogens and other microorganisms. We will discuss the implications of our results on local adaptation processes.

Keywords: seed microbiota, maternal effect, fungal community, forest pathogen, metabarcoding, Quercus.

O13. Geometagenomics illuminates the impact of agriculture on the distribution and prevalence of plant viruses at the ecosystem scale.

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Disease emergence events regularly result from human activities such as agriculture, which frequently brings large populations of genetically uniform hosts into contact with potential pathogens. Although viruses cause nearly 50% of emerging plant diseases, there is little systematic information about virus distribution across agro-ecological interfaces and large gaps in

understanding of virus diversity in nature. Here we applied a novel landscape-scale geometagenomics approach to examine relationships between agricultural land use and distributions of plant-associated viruses in two Mediterranean-climate biodiversity hotspots (Western Cape region of South Africa and Rhône river delta region of France). In total, we analysed 1725 geo-referenced plant samples collected over two years from 4.5 km x 4.5 km grids spanning farmlands and adjacent uncultivated vegetation. We found substantial virus prevalence (25.8–35.9%) in all ecosystems, but prevalence and identified family-level virus diversity were greatest in cultivated areas, with some virus families displaying strong agricultural associations. Our survey revealed 94 previously unknown virus species, primarily from uncultivated plants. This is the first effort to systematically evaluate plant-associated viromes across broad agro-ecological interfaces. Our findings indicate that agriculture substantially influences plant virus distributions and highlight the extent of current ignorance about the diversity and roles of viruses in nature.

Keywords: Spatial metagenomics, plant-associated viruses, Mediterranean agroecosystems

O14. The structure and genetics of cross-resistance evolution in bacteria-phage interactions.

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Antagonistic coevolution between bacteria and phage, resulting in reciprocal selection for improved resistance and infectivity, highly influences the structure of microbial communities. However, the impact of specific resistance mutations is dependent on the structure and degree of cross resistance between phage strains. We selected spontaneous resistance mutants of *Pseudomonas aeruginosa* against 27 phage strains individually to determine the structure, genetic basis and cost of cross-resistance. Whilst the magnitude of cross-resistance provided by mutations selected against different phage strains varied greatly, this was not limited by associated fitness costs, and demonstrates that broad resistance ranges can be selected even in the absence of multiple phage strains. Using network analysis to characterise the structure of cross-resistance within the phage collection, we identified two distinct phage groups, with high within- but low between-group cross-resistance. Examining resistance mutations, which provide only within-group cross-resistance revealed a distinct molecular target for each group; resistance mutations targeted type IV pilus within Group 1 and lipopolysaccharide biosynthesis within Group 2. More generalist resistance, providing between-group cross-resistance, was provided by mutations affecting *rpoN*, and alternative sigma factor, which controls expression of many lifestyle-associated traits including motility, biofilm formation and quorum sensing. Further, we showed that cross-resistance could predict the efficacy of phage cocktails, both in terms of the rate of resistance evolution and ability to suppress bacterial growth. These results suggest that cross-resistance is likely to be a common property of bacteria-phage communities, and that the structure of cross-resistance could strongly influence their structure and stability. Additionally, understanding these processes could greatly improve the treatment of bacterial infections, for example, limiting cross-resistance could drastically improve the rational design of phage therapy cocktails.

Keywords: Phage therapy, cross-resistance, experimental evolution

Pathobiome 2018

18th-20th March 2018 –

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